

(FILE 'HOME' ENTERED AT 15:14:16 ON 13 DEC 2005)

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 15:14:19 ON 13 DEC 2005

L1	2122 S PENICILLIUM (2N) CITRINUM
L2	79 S L1 AND (REDUCTASE OR OXIDOREDUCTASE)
L3	55 DUP REM L2 (24 DUPLICATES REMOVED)
L4	0 S L3 AND 325
L5	0 S L4 AND (MUTA OR VARI? OR MODIFI?)
L6	8 S L3 AND (MUTA OR VARI? OR MODIFI?)
L7	8 DUP REM L6 (0 DUPLICATES REMOVED)
L8	3 S L7 AND PY<2003

	Type	L #	Hits	Search Text
1	BRS	L1	17	"1386961"
2	BRS	L2	466	penicillium near2 citrinum
3	BRS	L3	11	l2 near10 reductase



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Limits: Publication Date to 2002

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- Search numbers may not be continuous; all searches are represented.
- Click on query # to add to strategy

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Search	Most Recent Queries	Time	Result
#12	Search penicillium citrinum reductase Field: All Fields , Limits: Publication Date to 2002	15:08:12	<u>11</u>
#11	Search penicillium citrinum reductase	15:07:59	<u>14</u>
#10	Search penicillium citrinum	15:07:53	<u>206</u>
#9	Search abid aird	13:50:24	<u>11</u>
#8	Search angiogenesis apocynin Limits: Publication Date to 2000	10:22:26	<u>1</u>
#6	Search angiogenesis aebsf Limits: Publication Date to 2000	10:21:14	<u>2</u>
#5	Search angiogenesis dpi Limits: Publication Date to 2000	10:21:07	<u>0</u>
#3	Search angiogenesis nadph oxidase Field: All Fields , Limits: Publication Date to 2000	10:19:29	<u>1</u>
#2	Search angiogenesis nadph oxidase	10:18:15	<u>26</u>
#1	Search angiogenesis nadph	10:18:11	<u>51</u>

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 ☒ MGC
 ☒ HPRD
 ☒ :

☐ 1: [CAF33259](#). Reports unnamed protein p...[gi:45112868] [BLink](#), [Links](#)

LOCUS CAF33259 325 aa linear PLN 04-MAR-2004
 DEFINITION unnamed protein product [Penicillium citrinum]..
 ACCESSION CAF33259
 VERSION CAF33259.1 GI:45112868
 DBSOURCE embl accession [CQ769141.1](#)
 KEYWORDS .
 SOURCE Penicillium citrinum
 ORGANISM [Penicillium citrinum](#)
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.

REFERENCE 1
 AUTHORS Asako,H. and Shimizu,M.
 TITLE Modified reductase and its gene and use thereof
 JOURNAL Patent: EP 1386961-A 04-FEB-2004;
 Sumitomo Chemical Company, Limited (JP)

FEATURES
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NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Range: from to ☐ Reverse complemented strand Features: ☐

☐ 1: [CQ769141](#). Reports Sequence 2 from P...[gi:45112867] [Links](#)

LOCUS CQ769141 978 bp DNA linear PAT 04-MAR-2004

DEFINITION Sequence 2 from Patent EP1386961.

ACCESSION CQ769141

VERSION CQ769141.1 GI:45112867

KEYWORDS .

SOURCE *Penicillium citrinum*

ORGANISM *Penicillium citrinum*
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Penicillium*.

REFERENCE 1

AUTHORS Asako,H. and Shimizu,M.

TITLE Modified reductase and its gene and use thereof

JOURNAL Patent: EP 1386961-A 2 04-FEB-2004;
Sumitomo Chemical Company, Limited (JP)

FEATURES

source Location/Qualifiers

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CDS 1..978

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ORIGIN

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Database : UniProt_05.80:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1514	87.5	325	2	Q877A2_ASPOR	Q877a2 aspergillus
2	1477	85.3	325	2	Q4WQ65_ASPFU	Q4wq65 aspergillus
3	1471	85.0	325	2	Q5B1L7_EMENI	Q5b1l7 aspergillus
4	1471	85.0	325	2	Q7Z8L1_EMENI	Q7z8l1 emericella
5	1205.5	69.6	331	2	Q7S3U4_NEUCR	Q7s3u4 neurospora
6	1191	68.8	327	2	Q6RZX1_TRIAT	Q6rzx1 trichoderma
7	1137.5	65.7	323	2	Q51QM9_MAGGR	Q51qm9 magnaporthe
8	1038	60.0	256	2	Q4I4F0_GIBZE	Q4i4f0 gibberella
9	1037	59.9	254	2	O74646_GIBZE	O74646 gibberella
10	635	36.7	355	2	Q4PHK0_USTMA	Q4phk0 ustilago ma
11	623	36.0	1224	2	Q4P7C0_USTMA	Q4p7c0 ustilago ma
12	602.5	34.8	332	2	Q4IEY5_GIBZE	Q4iey5 gibberella
13	595.5	34.4	309	2	Q55SW0_CRYNE	Q55sw0 cryptococcu
14	593.5	34.3	309	2	Q5KH94_CRYNE	Q5kh94 cryptococcu
15	583	33.7	310	2	Q6FR42_CANGA	Q6fr42 candida gla
16	575.5	33.2	310	2	Q6FY54_CANGA	Q6fy54 candida gla
17	574.5	33.2	312	1	GCY_YEAST	P14065 saccharomyc
18	570.5	33.0	309	2	Q6CRC8_KLULA	Q6crc8 kluyveromyc
19	568	32.8	321	1	YDG7_SCHPO	Q10494 schizosacch
20	565.5	32.7	325	2	Q5KLM8_CRYNE	Q5klm8 cryptococcu
21	563.5	32.6	325	2	Q55YB1_CRYNE	Q55yb1 cryptococcu
22	560.5	32.4	313	2	Q4X1E8_ASPFU	Q4x1e8 aspergillus
23	559.5	32.3	322	1	ALDX_SPOSA	P27800 sporobolomy
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- 1: geneseqp1980s:*
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- 3: geneseqp2000s:*
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- 5: geneseqp2002s:*
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- 8: geneseqp2004s:*
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SUMMARIES

Result No.	%		Query Match Length	DB	ID	Description
	Score	Query				
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2	1731	100.0	325	7	ADE39629	Ade39629 Penicilli
3	1731	100.0	325	8	ADH44214	Adh44214 Penicilli
4	1731	100.0	325	8	ADL18258	Adl18258 Penicilli
5	1731	100.0	325	8	ADK70247	Adk70247 Penicilli
6	1731	100.0	325	8	ADM46686	Adm46686 325 amino
7	1731	100.0	325	8	ADM46567	Adm46567 Penicilli
8	1731	100.0	325	8	ADK51190	Adk51190 Wild-type
9	1731	100.0	325	8	ADN97092	Adn97092 3 hydroxy
10	1728	99.8	325	8	ADK51203	Adk51203 Mutant Pe
11	1726	99.7	325	8	ADK51204	Adk51204 Mutant Pe
12	1723	99.5	325	8	ADK51205	Adk51205 Mutant Pe
13	972.5	56.2	255	8	ADN20743	Adn20743 Bacterial
14	575.5	33.2	312	2	AAW29220	Aaw29220 S. cerevi
15	574.5	33.2	312	2	AAW29217	Aaw29217 S. cerevi
16	574.5	33.2	312	4	AAG63565	Aag63565 Amino aci
17	574.5	33.2	312	5	ABG93198	Abg93198 S. cerevi
18	574.5	33.2	312	8	ADS43942	Ads43942 Bacterial
19	574.5	33.2	313	4	AAG63566	Aag63566 Synthetic
20	573.5	33.1	312	2	AAW29218	Aaw29218 S. cerevi
21	568	32.8	321	8	ADN19632	Adn19632 Bacterial

Same paper...

bad data

Database : Issued_Patents_AA:*

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- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1731	100.0	325	2	US-10-004-115B-1	Sequence 1, Appli
2	574.5	33.2	312	2	US-09-734-237B-42	Sequence 42, Appl
3	574.5	33.2	313	2	US-09-734-237B-44	Sequence 44, Appl
4	558.5	32.3	290	2	US-09-248-796A-17316	Sequence 17316, A
5	555	32.1	312	2	US-09-487-558B-438	Sequence 438, App
6	555	32.1	313	2	US-09-734-237B-39	Sequence 39, Appl
7	547.5	31.6	344	2	US-09-630-983A-20	Sequence 20, Appl
8	547	31.6	328	2	US-10-040-416-6	Sequence 6, Appli
9	545.5	31.5	328	2	US-10-040-416-4	Sequence 4, Appli
10	543.5	31.4	313	2	US-09-347-803-6	Sequence 6, Appli
11	541	31.3	322	2	US-09-734-237B-32	Sequence 32, Appl
12	538	31.1	330	2	US-10-040-416-2	Sequence 2, Appli
13	523.5	30.2	313	2	US-09-347-803-25	Sequence 25, Appl
14	518.5	30.0	308	2	US-09-347-803-10	Sequence 10, Appl
15	516	29.8	280	2	US-09-769-787-49	Sequence 49, Appl
16	509.5	29.4	309	2	US-09-347-803-14	Sequence 14, Appl
17	501.5	29.0	302	2	US-09-270-767-45294	Sequence 45294, A
18	501.5	29.0	310	2	US-09-166-412-4	Sequence 4, Appli
19	501.5	29.0	310	2	US-08-731-320B-4	Sequence 4, Appli
20	501.5	29.0	310	2	US-09-166-438-4	Sequence 4, Appli
21	499.5	28.9	316	2	US-08-801-344-4	Sequence 4, Appli

US-10-004-115B-1

; Patent No. 6884607

; APPLICANT: ASAKO, HIROYUKI

; APPLICANT: SHIMIZU, MASATOSHI

; APPLICANT: WAKITA, RYUHEI

; TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE

; CURRENT APPLICATION NUMBER: US/10/004,115B

; PRIOR APPLICATION NUMBER: JP 2000-372704

; PRIOR APPLICATION NUMBER: JP 2001-006144

; PRIOR APPLICATION NUMBER: JP 2001-026594

; PRIOR APPLICATION NUMBER: JP 2001-175175

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; NUMBER OF SEQ ID NOS: 37
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; SEQ ID NO 1

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; TYPE: PRT
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US-10-004-115B-1

DAM ena SID1
n variants

Best Local Similarity 100.0%; Pred. No. 3.3e-177;

Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Db

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 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	574.5	33.2	312	1	S22846	probable aldehyde
2	568	32.8	321	2	T38413	probable oxidoredu
3	559.5	32.3	323	2	S78113	aldehyde reductase
4	555	32.1	312	2	S61163	aldo-keto reductas
5	553	31.9	327	1	S76143	probable aldehyde
6	548.5	31.7	325	2	T39169	probable oxidoredu
7	547.5	31.6	344	1	S46020	probable aldehyde
8	529.5	30.6	309	2	A84599	hypothetical prote
9	529	30.6	290	2	T02543	aldehyde dehydroge
10	527.5	30.5	309	2	B84599	hypothetical prote
11	523.5	30.2	294	2	T02542	probable alcohol d
12	523.5	30.2	313	2	T09670	abscisic acid acti
13	521	30.1	320	2	T48188	aldose reductase-1
14	516	29.8	280	2	C98038	conserved hypothet
15	516	29.8	280	2	C95172	oxidoreductase, al
16	509	29.4	316	2	A37990	aldose reductase h
17	508.5	29.4	281	2	D86658	oxidoreductase ycg
18	503	29.1	276	2	C70040	plant-metabolite d
19	501.5	29.0	310	2	T17013	D-sorbitol-6-phosp
20	500	28.9	280	2	D69988	plant metabolite d
21	499.5	28.9	316	1	A60603	aldehyde reductase